

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 30, 2002, 17:24:00 ; Search time 11.84 Seconds

(without alignments)
366.266 Million cell updates/sec

Title: US-09-730-617-4

Perfect score: 568
Sequence: 1 MFGSLHFLAAGVPLSM.....LSRPAPQIQYRLVQLQK 112

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	94.2	121	1	NEUB_HUMAN
2	399	70.2	121	1	NEUB_MOUSE
3	152	26.8	32	1	NEUB_PIG
4	97.5	17.2	148	1	GRP_HUMAN
5	95.5	16.8	134	1	GRP_SHEEP
6	94	16.5	120	1	NEUB_XENLA
7	90.5	15.9	147	1	GRP_RAT
8	83	14.6	155	1	GRP_BOMOR
9	79.5	14.0	90	1	LITP_PHYSA
10	77.5	13.6	119	1	BOMB_BOMOR
11	74.5	13.1	2717	1	ZEPL_HUMAN
12	73.5	12.9	90	1	LITL_PHYSA
13	71.5	12.6	4303	1	PDOL_HUMAN
14	70	12.3	107	1	BOMB_BOMVA
15	70	12.3	339	1	PAX9_CHICK
16	69	12.1	145	1	RS23_YEAST
17	67.5	11.9	695	1	PID1_BOVIN
18	66.5	11.7	396	1	C121_MYCTU
19	66.5	11.7	756	1	PID1_RAT
20	66	11.6	82	1	RANA_RANPI
21	66	11.6	417	1	NTR2_MOUSE
22	65.5	11.5	1266	1	NGCA_CHICK
23	65	11.4	155	1	BCP_HAEN
24	64.5	11.4	327	1	YC29_SXNY3
25	64.5	11.4	423	1	HEM2_HUMAN
26	64.5	11.4	515	1	Y141_HUMAN
27	64.5	11.4	704	1	RP3A_BOVIN
28	64.5	11.4	1312	1	DPOL_PYRSD
29	64	11.3	143	1	RS23_SCHPO
30	63.5	11.2	392	1	WNM1_BOMMO
31	63.5	11.2	527	1	RAG2_MOUSE
32	63.5	11.2	639	1	NPT2_SHEEP
33	63.5	11.2	756	1	PID1_HUMAN

34	63	11.1	261	1	KLK2_HUMAN	P20151 homo sapien
35	63	11.1	478	1	ERG_CHICK	090837 gallus gall
36	63	11.1	535	1	C7C1_MATZE	043250 zea mays (m
37	62.5	11.0	416	1	NTR2_RAT	063384 ratius norv
38	62.5	11.0	1556	1	VG67_HSV11	000107 ictaluria h
39	62	10.9	330	1	Y374_METJA	057819 methanococ
40	62	10.9	2453	1	NCRI_MOUSE	060974 mus musculu
41	61.5	10.8	1654	1	PCFB_HUMAN	094913 homo sapien
42	61.5	10.8	2236	1	PYRI_DROME	P05990 drosophila
43	61	10.7	502	1	SYFA_YEAST	P15625 saccharomyc
44	61	10.7	554	1	YER2_YEAST	P40055 saccharomyc
45	60.5	10.7	227	1	AGL8_LYCESC	040170 lycopersico

ALIGNMENTS

RESULT	ID	NEUB_HUMAN	STANDARD	PRT	121 AA.
AC	P08949	096HH5	096A06		
DT	01-NOV-1988	(Rel. 09, Created)			
DT	01-MAR-2002	(Rel. 41, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Neuromedin B-32 precursor [Contains: Neuromedin B].				
GN	NMB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISUS-Hypothalamus;				
RX	MEDLINE=88330837; PubMed=2458345;				
RA	Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;				
RT	"Molecular cloning of cDNAs encoding the human bombesin-like peptide				
RT	neuromedin B. Chromosomal localization and comparison to cDNAs				
RT	encoding its amphibian homolog ranatensin."				
RL	J. Biol. Chem. 263:13317-13323(1988).				
RN	[2]				
RP	REVISED.				
RA	Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;				
RL	J. Biol. Chem. 265:7091-7091(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISUS-Brain, and ovary;				
RA	Strausberg R.;				
RL	Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: stimulates smooth muscle contraction in a manner similar				
CC	to that of bombesin.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be				
CC	produced by alternative splicing.				
CC	- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN				
CC	FAMILY.				
CC	-----				
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CC	-----				
CC	EMBL: M21551; AAA59934.1; -				
CC	EMBL: BC007407; AA074407.1; -				
CC	EMBL: BC007431; AA07431.1; -				
CC	EMBL: BC008603; AA08603.1; -				
CC	PIR: A28945; A28945.				
CC	MIM: 162340; -				
CC	InterPro: IPR000874; Bombesin.				
CC	Pfam: PF02044; Bombesin; 1.				
CC	PROSITE: PS00257; BOMBESIN; 1.				

Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 24
 FT PEPTIDE 25 56 NEUROMEDIN B-32.
 FT PEPTIDE 47 56 NEUROMEDIN B.
 FT PROPEP 60 121
 FT MOD_RES 56 36
 FT VARSPLIC 111 121
 FT CONFLICT 68 76
 FT SEQUENCE 121 AA: 13255 MW: 17FA0615486F03FB CRC64;
 SQ
 Query Match 94.2%; Score 535; DB 1; Length 121;
 Best Local Similarity 95.5%; Pred. No. 1.4e-50;
 Matches 107; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MGSLHFLALAGVYPLSWDPEPRSRASKIRVHSRGLMAGHMGKSLSPSPPL 60
 DB 10 MGSLHFLALAGVAPLSMDPEPRSRASKIRVHSRGLMAGHMGKSLSPSPPL 69
 QY 61 GRAPHTSLDQRLQSLHDLGILLKKALGVSLSPAPQIYRRLVQLQK 112
 DB 70 GRAPHTSLDQRLQSLHDLGILLKKALGVSLSPAPQIYRRLVQLQK 121
 RESULT 2
 NEUB_MOUSE STANDARD: PRT: 121 AA.
 AC 09CR53:
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Neuromedin B-32 precursor [contains: Neuromedin B].
 GN NMB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic head, and Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glasl C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombertis P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki K., Saito K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz K., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Stimulates smooth muscle contraction in a manner similar
 CC to that of bombesin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANNTENSIN
 CC FAMILY.
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 CC -----
 CC DR EMBL: AK014077; BAB29144.1; -;
 CC DR EMBL: AK011929; BAB27922.1; -;
 CC DR MGD: MGI:1915289; Nmb.
 CC DR InterPro: IPR000874; Bombesin.
 CC DR Pfam: PF02044; Bombesin; 1.
 CC DR PROSITE: PS00257; BOMBESIN; 1.
 CC KW Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT PEPTIDE 25 56 NEUROMEDIN B-32.
 FT PEPTIDE 47 56 NEUROMEDIN B.
 FT PROPEP 60 121
 FT MOD_RES 56 56
 FT SEQUENCE 121 AA: 13571 MW: 1EE94C96303D9D31 CRC64;
 SQ
 Query Match 70.2%; Score 399; DB 1; Length 121;
 Best Local Similarity 75.0%; Pred. No. 5.3e-36;
 Matches 81; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 QY 5 LHLFALLAGVYPLSWDPEPRSRASKIRVHSRGLMAGHMGKSLSPSPPLGTAP 64
 DB 14 LHLFALLAGVAPFNMWDLPEPRSRASKIRVHPRGNLMATGHMGKSLSPSLVGTAP 73
 QY 65 HTSLRQRLQSLHDLGILLKKALGVSLSPAPQIYRRLVQLQK 112
 DB 74 PHTPRQRLQSLHDLRLILRRKALGMNPSGPAPQIYRRLVQLQK 121
 RESULT 3
 NEUB_PIG STANDARD: PRT: 32 AA.
 AC P01297;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Neuromedin B-32 [contains: Neuromedin B].
 GN NMB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85279454; PubMed=4026853;
 RA Minamino N., Sudoh T., Kangawa K., Matsuo H.,
 RA "Neuromedin B-32 and B-30: two 'big' neuromedin B identified in
 RT porcine brain and spinal cord.";
 RL Biochem. Biophys. Res. Commun. 130:685-691(1985).
 RN [2]
 RP SEQUENCE.
 RA Minamino N., Kangawa K., Matsuo H.,
 RT "Neuromedin B and neuromedin C: two mammalian bombesin-like peptides
 RT identified in pig spinal cord and brain.";
 RL Regul. Pept. 19:127-127(1987).
 RN [3]
 RP SEQUENCE OF 23-32.
 RX MEDLINE=83282813; PubMed=6882442;
 RA Minamino N., Kangawa K., Matsuo H.,
 RT "Neuromedin B: a novel bombesin-like peptide identified in porcine
 RT spinal cord.";
 RL Biochem. Biophys. Res. Commun. 114:541-548(1983).
 CC -1- FUNCTION: Stimulates smooth muscle contraction in a manner similar
 CC to that of bombesin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANNTENSIN
 CC FAMILY.
 CC PIR: B60301; BSPGNB.

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DR EMBL: S75723; AAB32675.1; -
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin; 1.
 DR PROSITE: PS00257; BOMBESIN; 1.
 DR Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT PEPTIDE 24 50 GASTRIN-RELEASING PEPTIDE.
 FT PROPEP 54 134
 FT PEPTIDE 41 50 NEUROMEDIN C.
 FT MOD_RES 50 50 AMIDATION (G-5) PROVIDE AMIDE GROUP).
 FT SEQUENCE 134 AA; 14655 MW; C8958538E4C6F044 CRC64;

Query Match 16.8%; Score 95.5; DB 1; Length 134;
 Best Local Similarity 29.8%; Pred. No. 0.0021;
 Matches 28; Conservative 17; Mismatches 30; Indels 19; Gaps 3;

OY 23 PEPRSRASKI-----RVHSRCKLWAIHFHMGKSLSPSPPLGTAPHTSLRD--Q 71
 DB 17 PAPRCSAAPVTAGACALAKMYTRGNHMAVGLMGKKSVAESPQLREESLKEQREYVQ 76
 OY 72 RQLSHDLGILLKALG-----VSLSRPA 97
 DB 77 WEATRNLLSLQAKVAGQHPPNPEPLSHQPA 110

RESULT 6

NEUB_XENLA STANDARD: PRT: 120 AA.

AC P43443;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Neuromedin B precursor.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93028554; PubMed=1409705;
 RA Wechsberger C., Kreil G., Richter K.;
 RT *Isolation and sequence of a cDNA encoding the precursor of a
 RT bombesin-like peptide from brain and early embryos of Xenopus
 RT laevis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9819-9822(1992).
 CC -1- FUNCTION: MAY BE A GROWTH FACTOR REQUIRED FOR THE HIGH RATE OF
 CC CELL DIVISION ENSURING AFTER FERTILIZATION, OR MAY HAVE A ROLE AS A
 CC SECRETAGOGUE THAT TRIGGERS THE RELEASE OF STORED COMPONENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: BRAIN, INTESTINE, AND OVARIES AND EARLY
 CC EMBRYOS (STAGES 2 AND 10).
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.
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DR EMBL: L01530; AAA49912.1; -
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin; 1.
 DR PROSITE: PS00257; BOMBESIN; 1.
 DR Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 44
 FT PEPTIDE 45 54 NEUROMEDIN B.
 FT PROPEP 58 120
 FT MOD_RES 54 54 AMIDATION (G-55 PROVIDE AMIDE GROUP).
 FT SEQUENCE 120 AA; 14384 MW; 2CB146BA082A2442 CRC64;

Query Match 16.5%; Score 94; DB 1; Length 120;
 Best Local Similarity 45.6%; Pred. No. 0.0026;
 Matches 26; Conservative 7; Mismatches 16; Indels 8; Gaps 4;

OY 5 LHFALLAGVPLSM--DLPEPRSRASKIRVHSRCKLWAIHFHMGKSLSPS-SPS 58
 DB 15 LTHLLLS--FLPYLCMEFSEDARNIEKIR--RGNQWAIHFHMGKSLDPTNPS 66

RESULT 7

GRP_RAT STANDARD: PRT: 147 AA.

AC P24393;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Gastrin-releasing peptide precursor (GRP) [contains: Neuromedin C
 DE (GRP-10)].
 GN GRP.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=86334558; PubMed=2843761;
 RA Lebacqz-Verheyden A.M., Krystal G., Sartor O., May J., Batley J.F.;
 RT "The rat prepro gastrin releasing peptide gene is transcribed from
 RT two initiation sites in the brain.";
 RL Mol. Endocrinol. 2:556-563(1988).
 CC -1- FUNCTION: GRP stimulates gastrin release as well as other
 CC gastrointestinal hormones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.
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DR EMBL: M31176; AAA41197.1; -
 DR PIR: A40922; A40922.
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin; 1.
 DR PROSITE: PS00257; BOMBESIN; 1.
 DR Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 23
 FT PEPTIDE 24 52 GASTRIN-RELEASING PEPTIDE.
 FT PROPEP 56 147
 FT PEPTIDE 43 52 NEUROMEDIN C.
 FT MOD_RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).
 FT SEQUENCE 147 AA; 15817 MW; D6AF30B45DBAFCIF CRC64;

Query Match 15.9%; Score 90.5; DB 1; Length 147;
 Best Local Similarity 28.8%; Pred. No. 0.0079;
 Matches 34; Conservative 16; Mismatches 39; Indels 29; Gaps 5;

QY 1 MFGSLHFAALLAGVPLSWDLPPEPRSRASKI-----RVHSRGLMAIGHFNGK 49
 DB 1 MRGSELSTLLALVL-----CQAPRGPAVPSTGAGGTVLAKMYPRGSHWAVGHLMGK 54
 QY 50 KSLPESSSPGLGTAPHNSLRDRL-----QLSHDLGLILLKALGVSLSRPAPO 101
 DB 55 KSTD-ELPLLYAADRDGLKQLNGYLRMEBAARLLGLEASR---NRSHQPPQD 106

RESULT 8

GRP_BOMOR STANDARD; PRT; 155 AA.
 AC P29007;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Gastrin-releasing peptide precursor (GRP-29) [Contains: Neuromedin C (GRP-10); C-terminal extension peptide (CTEP)].
 OS Bombina orientalis (Oriental fire-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8346;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 51-60.
 RC TISSUE=Gut;

RA Nagalla S.R., Gibson B.W., Tang D., Reeve J.R. Jr., Spindel E.R.;
 RT "Gastrin-releasing peptide (GRP) is not mammalian bombesin.
 RT Identification and molecular cloning of a true amphibian GRP distinct
 RT from amphibian bombesin in Bombina orientalis.";
 RL J. Biol. Chem. 267:6916-6922(1992).
 CC -1- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER
 CC GASTROINTESTINAL HORMONES. MAY HAVE A ROLE AS NEUROTRANSMITTER OR
 CC NEUROMODULATOR.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: BRAIN AND STOMACH. IN THE STOMACH GRP WAS
 CC LOCALIZED, AT THE BASE OF THE GASTRIC PITS, TO OCCASIONAL CELLS
 CC WHOSE DISTRIBUTION AND APPEARANCE WERE CONSISTENT WITH THAT OF
 CC GUT NEUROENDOCRINE CELLS.

CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RAANTENSIN
 CC FAMILY.

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CC -----
 CC EMBL: M83737; AAA51409.1; -;
 DR PTR: A42437;
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin; 1.
 DR PROSITE: PS00257; BOMBESIN; 1.
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL. 1 31
 FT PEPTIDE 32 60 GASTRIN-RELEASING PEPTIDE.
 FT PEPTIDE 51 60 NEUROMEDIN C.
 FT PEPTIDE 64 125 C-TERMINAL EXTENSION PEPTIDE (POTENTIAL).
 FT PROPEP 128 155
 FT MOD_RES 60 60 AMIDATION (G-61 PROVIDE AMIDE GROUP).
 FT MOD_RES 155 AA: 17813 MW: 8972A6E05AC474F CRC64;
 SQ SEQUENCE

Query Match 14.6%; Score 83; DB 1; Length 155;
 Best Local Similarity 40.7%; Pred. No. 0.054;

Matches 22; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

QY 6 LHFALLAGV---VPLSWDLP---EPRSRASKIRVHSGKLMATIGHFNGKSKLE 53
 DB 13 LFFVLVCSLVLCVKYHLSQLAPTSQOHNDASLSKIYPRGSHWAVGHLMGKSKLE 66

RESULT 9

LITP_PHYSA STANDARD; PRT; 90 AA.
 ID LITP_PHYSA
 AC P08947;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phe(8)-phylloleptin precursor.
 OS Phyllomedusa sauvagii (Sauvage's leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Phyllomedusa.
 OX NCBI_TaxID=8395;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95089778; PubMed=7997236;
 RA Nagalla S.R., Barry B.J., Spindel E.R.;
 RT "Cloning of complementary DNAs encoding the amphibian bombesin-like
 RT peptides Phe8 and leu8 phylloleptin from Phyllomedusa sauvagii:
 RT potential role of U to C RNA editing in generating neuropeptide
 RT diversity.";
 RL Mol. Endocrinol. 8:943-951(1994).
 RN [2]

RP SEQUENCE OF 49-57.
 RX MEDLINE=86177052; PubMed=3868775;
 RA Erspamer V., Melchiorri P., Erspamer G.F., Montecucci P.C.;
 RA de Castiglione R.;
 RT "Phyllomedusa skin: a huge factory and store-house of a variety of
 RT active peptides.";
 RL Peptides 6 Suppl. 3:7-12(1985).
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RAANTENSIN
 CC FAMILY.

CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: S77226; AAB32788.1; -;
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin; 1.
 DR PROSITE: PS00257; BOMBESIN; 1.
 KW Bombesin family; Amidation; Signal.
 FT SIGNAL. 1 30
 FT PROPEP 31 48
 FT PEPTIDE 49 57 PHE[8]-PHYLLOLEPTIN.
 FT PEPTIDE 61 90
 FT MOD_RES 49 49 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 57 57 AMIDATION (G-58 PROVIDE AMIDE GROUP).
 FT MOD_RES 57 57
 SQ SEQUENCE 90 AA: 10147 MW: 0BACB3400ICACE3C CRC64;

Query Match 14.0%; Score 79.5; DB 1; Length 90;
 Best Local Similarity 41.2%; Pred. No. 0.066;
 Matches 21; Conservative 6; Mismatches 23; Indels 1; Gaps 1;

QY 3 GSLEHFAALLAGVPLSWDLPPEPRSRASKIRVHSGKLMATIGHFNGKSKLE 53
 DB 14 GFLAHLSTFVTLTVCKEVEESDLSKRNVLOR-QLMAVSPFGKSKLE 63

RESULT 10

BOMB_BOMOR STANDARD; PRT: 119 AA.

ID BOMB_BOMOR

AC P21591;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Bombesin precursor.

OS Bombina orientalis (Oriental fire-bellied toad).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.

OX NCBI_TaxID=8346;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-91088602; PubMed-2263631;

RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;

RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship between bombesin and gastrin-releasing peptide.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).

CC -1- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION, ROLE IN INDUCTION OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY GASTROINTESTINAL HORMONES.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN THE SKIN AND THE BRAIN.

CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANNTENSIN FAMILY.

CC -----

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CC -----

DR EMBL: M55255; AAA48551.1; .

DR PIR: A39261; A39261.

DR InterPro: IPR000874; Bombesin.

DR Pfam: PF02044; Bombesin; 1.

DR PROSITE: PS00257; BOMBESIN; 1.

KW Bombesin family; Amidation; Cleavage on pair of basic residues;

KW SIGNAL.

FT SIGNAL 1 29 POTENTIAL.

FT PROPEP 30 44

FT PEPTIDE 45 58 BOMBESIN.

FT PROPEP 62 119

FT MOD_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).

SO SEQUENCE 119 AA; 13863 MW; 3A3D84EA245A44A CRC64;

Query Match 13.6%; Score 77.5; DB 1; Length 119;

Best Local Similarity 30.3%; Pred. No. 0.15;

Matches 23; Conservative 13; Mismatches 35; Indels 5; Gaps 3;

OY 3 GLLHFPALLACVPLS--WDLPEPRASRKRVHSR-GKLMALGHFGKSLSPSSSP 59

DB 13 GFLFH--LLIFSFLSSSCMEVEPDNNGRISLQDLGNQAVGHGKSLQDTDFEE 70

OY 60 LCTAPHTSLRDQQLQ 75

DB 71 MESFAKRVENKRAAL 86

RESULT 11

ZEPL_HUMAN STANDARD; PRT: 2717 AA.

ID ZEPL_HUMAN

AC P15822;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-Ep1) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)

DE (PRDII-BF1).

GN HIVEP1 OR ZNF40.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-90169514; PubMed-2106471;

RA Fan C.M., Maniatis T.;

RT "A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";

RL Genes Dev. 4:29-42(1990).

RM [2]

RP STRUCTURE BY NMR OF 2113-2142.

RX MEDLINE-91064333; PubMed-2248949;

RA Omichinski J.G., Clore G.M., Appella E., Sakaguchi K., Gronenborn A.M.;

RT "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution.";

RL Biochemistry 29:9324-9334(1990).

RM [3]

RP STRUCTURE BY NMR OF 2087-2142.

RX MEDLINE-92232684; PubMed-1567844;

RA Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E., Gronenborn A.M.;

RT "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1.";

RL Biochemistry 31:3907-3917(1992).

CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTGC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT IN T-CELL ACTIVATION.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- INDUCTION: BY MITOGEN AND PHORBOL ESTER.

CC -1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWEEN.

CC -1- SIMILARITY: STRONG TO HIVEP2.

CC -----

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CC -----

DR EMBL: X51435; CAA35798.1; .

DR PIR: A34203; A34203.

DR PDB: 3ZNF; 15-JAN-92.

DR PDB: 4ZNF; 15-JAN-92.

DR PDB: 1BBO; 31-OCT-93.

DR TRANSFAC: T00497; .

DR MIM: 194540; .

DR InterPro: IPR000822; ZNF-C2H2.

DR Pfam: PF00096; ZF-C2H2; 5.

DR PRINTS: PR00048; ZINC2FINGER.

DR SMART: SM00355; ZNF_C2H2; 4.

DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.

DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 4.

KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; 3D-structure.

KW DOMAIN

FT DOMAIN 406 456 ZINC_FINGERS.

FT ZN_FING 406 428 C2H2-TYPE.

FT ZN_FING 434 456 C2H2-TYPE.

FT DOMAIN 803 806 POLY-SER.

FT ZN_FING 958 981 C2HC-TYPE (POTENTIAL).

FT DOMAIN 2087 2139 ZINC_FINGERS.

FT ZN_FING 2087 2109 C2H2-TYPE.

FT 2N_FING 2115 2139 C2H2-TYPE.
 FT STRAND 2088 2088
 FT TURN 2090 2092
 FT STRAND 2095 2095
 FT HELIX 2099 2108
 FT TURN 2109 2109
 FT STRAND 2115 2116
 FT STRAND 2123 2124
 FT HELIX 2127 2135
 SQ SEQUENCE 2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;

Query Match 13.1%; Score 74.5; DB 1; Length 2717;
 Best Local Similarity 38.4%; Pred. No. 14;
 Matches 28; Conservative 5; Mismatches 23; Indels 17; Gaps 3;

OY 17 PLSDLDPEPRASKI-----RVHSRGLWAIGHFMGKSLSPSPGLCTAPHTSLRD 70
 DB 1144 PNFDPKPEPRASPVSPFOELNRGNSGLKVG-----ISQESHPSRDSGSHPH----- 1193
 OY 71 QRLQSLDLGL 83
 DB 1194 -QALSDALRGEL 1205

RESULT 12

LITL_PHYSA STANDARD; PRT: 90 AA.
 ID LITL_PHYSA
 AC P08948;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Leu[8]-phyllolitorin precursor.
 OS Phyllomedusa sauvagei (Sauvage's leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Phyllomedusa.
 ON NCBI_Taxid=8395;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95089778; PubMed=7997236;
 RA Negalla S.R., Barry B.J., Spindel E.R.;
 RT "Cloning of complementary DNAs encoding the amphibian bombesin-like
 RT peptides Pheb and Leu8 phyllolitorin from Phyllomedusa sauvagei:
 RT potential role of U to C RNA editing in generating neuropeptide
 RT diversity.";
 RL Mol. Endocrinol. 8:943-951(1994).
 RN [2]
 RP SEQUENCE OF 49-57.
 RX MEDLINE=86177052; PubMed=3868775;
 RA Erspamer V., Melchiorri P., Erspamer G.F., Montecucchi P.C.;
 RA "de Castiglione R.;
 RT "Phyllomedusa skin: a huge factory and store-house of a variety of
 RT active peptides.";
 RL Peptides 6 Suppl. 3:7-12(1985).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: S77208; AAB32787.1; -;
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin.1.
 DR PROSITE: PS00257; BOMBESIN.1.
 KW Bombesin family; Amidation; Signal.
 FT SIGNAL 1 30 POTENTIAL.

FT PROPER 31 48
 FT PEPTIDE 49 57 LEU[8]-PHYLLOLITORIN.
 FT PROPER 61 90
 FT MOD_RES 49 49 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 57 57 AMIDATION (G-58 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 90 AA; 10113 MW; 0BACBD4EE124CE3C CRC64;

Query Match 12.9%; Score 73.5; DB 1; Length 90;
 Best Local Similarity 39.2%; Pred. No. 0.29;
 Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

OY 3 GSLHFAALLAGVPLSDLDPEPRASKIRVHSGRLWAIGHFMGKSLSE 53
 DB 14 GFLAHLLSTVYTLVTCKEVTEESDLSKRVLQR-QLMVAGSLMGKSLSE 63

RESULT 13

PKDL_HUMAN STANDARD; PRT: 4303 AA.
 ID PKDL_HUMAN
 AC P98161;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Polycystin precursor (Autosomal dominant polycystic kidney disease
 DE protein 1).
 GN PKDL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95254638; PubMed=7736581;
 RA Glucksmann-Kuiss M.A., Tayber O., Woolf E.A., Bougueleret L.,
 RA Deng N., Alperin G.D., Iris F., Hawkins F., Munro C., Lakey N.,
 RA Duyk G., Schneider M.C., Geng L., Zhang F., Zhao Z., Torosian S.,
 RA Readers S.T., Bork P., Pohlshmidt M., Loehning C., Kraus B.,
 RA Nowicka U., Leung A.L.S., Frischmidt A.-M.;
 RT "Polycystic kidney disease: the complete structure of the PKD1 gene
 RT and its protein.";
 RL Cell 81:289-298(1995).
 RN [2]
 RP SEQUENCE OF 2769-4303 FROM N.A.
 RX MEDLINE=94273192; PubMed=8004675;
 RA Ward C.J., Peral B., Hughes J., Thomas S., Gamble V.,
 RA MacCarthy A.B., Sloane-Stanley J., Buckle V.J., Kearney L.,
 RA Higgs D.R., Ratcliffe P.J., Harris P.C., Roeliffsema J.H.,
 RA Spruit L.L., Sarris J.J., Dauwerse H.G., Peters D.J.M.,
 RA Breuning M.H., Nellist M., Brook-Carter P.T., Maheshwar M.M.,
 RA Cordelero I., Santos H., Cabral P., Sampson J.R., Jansen B.,
 RA Hesselink-Jansen A.L.W., van den Ouweland A.K.W., Bussen B.,
 RA Verhoef S., Lindhout D., Hailey D.J.J.;
 RT "The polycystic kidney disease 1 gene encodes a 14 kb transcript and
 RT lies within a duplicated region on chromosome 16. The European
 RT Polycystic Kidney Disease Consortium.";
 RL Cell 77:881-894(1994).
 RN [3]
 RP STRUCTURE BY NMR OF 275-354.
 RX MEDLINE=99107746; PubMed=9889186;
 RA Bycroft M., Bateman A., Clarke J., Hamill S.J., Sandford R.,
 RA Thomas R.L., Chothia C.;
 RT "The structure of a PKD domain from polycystin-1: implications for
 RT polycystic kidney disease.";
 RL EMBO J. 18:297-305(1999).
 RN [4]
 RP VARIANT ADPKD 3748-ARG--VAL-752 DEL. AND VARIANT ASP-3632.
 RX MEDLINE=96108969; PubMed=8554072;
 RA Peral B., San Millan J.L., Ong A.C.M., Gamble V., Ward C.J.,
 RA Strong C., Harris P.C.;
 RT "Screening the 3' region of the polycystic kidney disease 1 (PKD1)
 RT gene reveals six novel mutations.";
 RL Am. J. Hum. Genet. 58:86-96(1996).

[5]
 RP VARIANTS ADPKD P-2993; R-3016 AND V-3511, AND VARIANTS M-3510 AND
 RP F-4190.
 RA MEDLINE-97342914; PubMed=9199561;
 RA Petrel B., Gamble V., Strong C., Ong A.C.M., Sloane-Stanley J.,
 RA Zervas K., Winearls C.G., Harris P.C.;
 RT "Identification of mutations in the duplicated region of the
 RT polycystic kidney disease 1 gene (PKD1) by a novel approach.";
 RL Am. J. Hum. Genet. 60:1399-1410(1997).
 RN [6]
 RP VARIANT ALA-4058.
 RA MEDLINE-97295081; PubMed=9150733;
 RA Constantinides R., Xenophontos S.L., Neophytou P., Nomura S.,
 RA Pterides A., Constantinou-Deltas C.D.;
 RT "New amino acid polymorphism, Ala/Val4058, in exon 45 of the
 RT polycystic kidney disease 1 gene: evolution of alleles.";
 RL Hum. Genet. 99:644-647(1997).
 RN [7]
 RP VARIANTS T-2760; P-2761; V-2763; T-2764; Q-2791; T-2826; L-3008 AND
 RP L-3064.
 RA MEDLINE-97449169; PubMed=9285784;
 RA Watnick T.J., Plontek K.B., Cordal T.M., Weber H., Gandolph M.A.,
 RA Qian F., Lens X.M., Neumann H.P.H., Germlo G.G.;
 RT "An unusual pattern of mutation in the duplicated portion of PKD1 is
 RT revealed by use of a novel strategy for mutation detection.";
 RL Hum. Mol. Genet. 6:1473-1481(1997).
 RN [8]
 RP VARIANT ADPKD THR-3678.
 RA MEDLINE-97403939; PubMed=9259200;
 RA Turco A.E., Rossetti S., Bresin E., Englisch S., Corra S.,
 RA Pignatelli P.F.;
 RT "Three novel mutations of the PKD1 gene in Italian families with
 RT autosomal dominant polycystic kidney disease.";
 RL Hum. Mutat. 10:164-167(1997).
 RN [9]
 RP VARIANT ADPKD ASP-4032, AND VARIANT VAL-4045.
 RA MEDLINE-98180892; PubMed=9521593;
 RA Davelis C., Maheshwar M.M., Lazarou L., Davies F., Coles G.,
 RA Rayne D.;
 RT "Novel and recurrent mutations in the PKD1 (polycystic kidney
 RT disease) gene.";
 RL Hum. Genet. 102:216-220(1998).
 RN [10]
 RP VARIANT ADPKD MET-3375.
 RA MEDLINE-99118881; PubMed=9921908;
 RA Koplides M., Constantinides R., Kyriakides G., Hadjigavriel M.,
 RA Patellis P.C., Pterides A., Deltas C.C.;
 RT "Loss of heterozygosity in polycystic kidney disease with a missense
 RT mutation in the repeated region of PKD1.";
 RL Hum. Genet. 103:709-717(1998).
 RN [11]
 RP VARIANTS ADPKD L-324 AND S-845, AND VARIANTS R-1399 AND L-1786.
 RA MEDLINE-99294580; PubMed=10364515;
 RA Thomas R.L., McConnell R., Whitlacker J., Kirkpatrick P., Bradley J.,
 RA Sandford R.;
 RT "Identification of mutations in the repeated part of the autosomal
 RT dominant polycystic kidney disease type 1 gene, PKD1, by long-range
 RT PCR.";
 RL Am. J. Hum. Genet. 65:39-49(1999).
 RN [12]
 RP VARIANTS ADPKD P-2392 AND F-2423, AND VARIANTS R-1399; Q-2548 AND
 RP R-2638.
 RA PubMed=10577909;
 RA Watnick T., Plantekeitchaen B., Johnson A., Gandolph M., Wang M.,
 RA Briefel G., Ringer K.W., Kimberling W., Gabow P., Germlo G.G.;
 RT "Mutation detection of PKD1 identifies a novel mutation common to
 RT three families with aneurysms and/or very-early-onset disease.";
 RL Am. J. Hum. Genet. 65:1561-1571(1999).
 RN [13]
 RP VARIANTS ADPKD L-3994--F-3996 DUPL; G-4136 AND C-4154, AND VARIANTS.
 RA MEDLINE-20441957; PubMed=10987650;
 RA Perichot R.A., Mercier B., Simon P.M., Whebe B., Cleides J., Ferec C.;
 RT "DGE screening of PKD1 gene reveals novel mutations in a large cohort

RT of 146 unrelated patients.";
 RL Hum. Genet. 105:231-239(1999).
 RN [14]
 RP VARIANTS ADPKD 3748-R--V-3752 DEL AND L-4132 DEL, AND VARIANT V-4045.
 RA MEDLINE-20112427; PubMed=10647901.
 RA Afzal A.R., Hand M., Ternes-Pereira E., Sagar-Malik A., Taylor R.,
 RA Jeffery S.;
 RT "Novel mutations in the 3 region of the polycystic kidney disease 1
 RT (PKD1) gene.";
 RL Hum. Genet. 105:648-653(1999).
 RN [15]
 RP VARIANTS ADPKD PRO-4225 AND TRP-4276.
 RA MEDLINE-99217041; PubMed=10200984;
 RA Badenas C., Torra R., San Millan J.L., Lucero L., Milla M.,
 RA Estivill X., Darnell A.;
 RT "Mutation analysis within the 3' region of the PKD1 gene.";
 RL Kidney Int. 55:1225-1233(1999).
 RN [16]
 RP VARIANTS ADPKD MET-2250 AND TRP-2329, AND VARIANTS CYS-2379; LEU-3066;
 RP VAL-3139 AND LEU-3193.
 RA MEDLINE-20311156; PubMed=10854095;
 RA Perichot R., Mercier B., Quere I., Carre A., Simon P., Whebe B.,
 RA Cleides J., Ferec C.;
 RT "Novel mutations in the duplicated region of PKD1 gene.";
 RL Eur. J. Hum. Genet. 8:353-359(2000).
 RN [17]
 RP VARIANTS ADPKD PRO-2921 AND MET-3375, AND VARIANT LEU-3066.
 RA MEDLINE-20382887; PubMed=10923040;
 RA Koplides M., Mean R., Demetrio K., Constantinides R., Pterides A.,
 RA Agiari G., Savelli S., Garbo M., Bozza A., Angello G., Penolazzi L.,
 RA De Paoli Vitelli E., La Torre C., Cappelli G., Piva R., del Seno L.;
 RT "Novel splicing and missense mutations in autosomal dominant
 RT polycystic kidney disease 1 (PKD1) gene: expression of mutated
 RT genes.";
 RL Hum. Mutat. 16:444-445(2000).
 RN [19]
 RP VARIANTS ADPKD SER-1166; GLU-1956; CYS-2408 AND GLY-2442--2443 INS,
 RP AND VARIANTS HIS-1995 AND ASN-2604.
 RA MEDLINE-20467506; PubMed=11012875;
 RA Plantekeitchaen B., Watnick T.J., Ahn C., Whang D.-Y., Burkhardt B.,
 RA Germlo G.G.;
 RT "Thirteen novel mutations of the replicated region of PKD1 in an Asian
 RT population.";
 RL Kidney Int. 58:1400-1412(2000).
 RN [20]
 RP VARIANTS ADPKD TRP-3753 AND ASN-3815.
 RA MEDLINE-20275386; PubMed=10729710;
 RA Kim U.R., Jin D.K., Ahn C., Shin J.H., Lee K.B., Kim S.H., Chae J.J.,
 RA Hwang D.Y., Lee J.G., Namkoong Y., Lee C.C.;
 RT "Novel mutations of the PKD1 gene in Korean patients with autosomal
 RT dominant polycystic kidney disease.";
 RL Mutat. Res. 432:39-45(2000).
 RN [21]
 RP VARIANTS ADPKD Q-13; F-75; C-139; 1992-F-T-1993 DELINS L; 2220-R--P-
 RP 2224 DEL; D-2336; D-2752; 2762-ILMR-2765 DUPL; M-2768; K-2771; P-2816;
 RP S-2858; 3012-W--Y-3017 DEL AND 3748-L--R-3752 DEL, AND VARIANTS S-
 RP 2674; M-2708; T-2734; L-2735; C-2765; M-2782; R-2814; G-2888; I-2905;
 RP D-2966 AND L-3066.
 RA MEDLINE-21063179; PubMed=11115377;
 RA Rossetti S., Strimecki L., Gamble V., Burton S., Sneddon V., Petrel B.,
 RA Roy S., Bakaloglu A., Komel R., Winearls C.G., Harris P.C.;
 RT "Mutation analysis of the entire PKD1 gene: genetic and diagnostic
 RT implications.";
 RL Am. J. Hum. Genet. 68:46-63(2001).
 RN [22]

Query Match 12.6%; Score 71.5; DB 1; Length 4303;
 Best Local Similarity 26.0%; Pred. No. 50;
 Matches 34; Conservative 17; Mismatches 51; Indels 29; Gaps 5;

QY 3 GSLHFAALLAGVDP-----LSMDLPEPRSRASRIRV---HSRKLMAIGHFMKRSLE 53
 DB 3133 GTTAHVAGTLMYGVDSRGSRHLDGDRAFHRNSLDIFRIATPHSGSVWKIRVWHDNKG- 3191
 QY 54 PSSSPPLGTAHTSTLRDOR-----LQSLHDLGLITLLKALGVSLSPAPQIQ 101
 DB 3192 ----SPAFLOHVIVRDLQTAARSAPFLVNDMLSVETANGGLVEKEVLAAS---DAALLR 3244
 QY 102 YRLLVLOILOK 112
 DB 3245 FRLLLVAELOK 3255

RESULT 14
 BOMB_BOMVA
 ID BOMB_BOMVA STANDARD: PRT: 107 AA.
 AC P01296; 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Bombesin precursor.
 OS Bombina variegata (Yellow-bellied toad), and
 OS Bombina bombina (Fire-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
 NX NCBI_TaxID=8348, 8345;
 RN 11
 RP SEQUENCE FROM N.A.
 RC SPECIES-B.variegata, TISSUE-Skin;
 RX MEDLINE=90242964; PubMed=2335218;
 RA Richter K., Egger R., Krell G.;
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin
 RT of Bombina variegata.";
 RL FEBS Lett. 262:353-355(1990).
 RN 12
 RP SEQUENCE OF 42-55.
 RC SPECIES-B.variegata, and B.bombina;
 RX MEDLINE=72163516; PubMed=4537042;
 RA Anastasi A., Erspamer V., Bucchi M.;
 RT "Isolation and amino acid sequences of alytesin and bombesin, two
 RT analogous active tetradecapeptides from the skin of European
 RT discoglossid frogs.";
 RL Arch. Biochem. Biophys. 148:443-446(1972).
 CC -1- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION, ROLE IN INDUCTION
 CC OF HYROTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY
 CC GASTROINTESTINAL HORMONES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X52447; CA636686.1; -;
 DR PIR: A01564; BSTD.
 DR PIR: B01564; BSTD.
 DR PIR: S09095; S09095.
 DR InterPro: IPR000874; Bombesin.
 DR Pfam: PF02044; Bombesin.1.
 DR PROSITE: PS00257; BOMBESIN.1.
 KM Bombesin family; Amidation; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL 1 26 POTENTIAL.

FT PROPEP 27 41
 FT PEPTIDE 42 55 BOMBESIN.
 FT PROPEP 56 107
 FT MOD_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 107 AA; 12341 MW; 9692B5060FAF618 CRC64;

Query Match 12.3%; Score 70; DB 1; Length 107;
 Best Local Similarity 22.7%; Pred. No. 0.85;
 Matches 25; Conservative 22; Mismatches 43; Indels 20; Gaps 4;

QY 3 GSLHFAALLAGVDP-----LSMDLPEPRSRASRIRVHSR-GKLMALIGHFMKRSLEPSPPLG 61
 DB 13 GFLLFSPFS---LSSCFEVEDPNNQGLNQQQLGNOMAVGHLGKRSLODTPFEKME 69
 QY 62 TAPHTSLRDORLQSLHDLGLITLLKALGVSLSPAPQIOYRRLVLOILO 111
 DB 70 SFAKRNVENMKASEREL-----RHA-QLVVRNILEOYLK 103

RESULT 15
 PAX9_CHICK
 ID PAX9_CHICK STANDARD: PRT: 339 AA.
 AC P55166;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Paired box protein PAX-9 (Fragment).
 GN PAX9.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NX NCBI_TaxID=9031;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96427393; PubMed=8812138;
 RA Mueller T.S., Ebensperger C., Neubueser A., Koseki H., Balling R.,
 RA Christ B., Witting J.;
 RT "Expression of avian Pax1 and Pax9 is intrinsically regulated in the
 RT pharyngeal endoderm, but depends on environmental influences in the
 RT paraxial mesoderm.";
 RL Dev. Biol. 178:403-417(1996).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
 CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X92652; CA63343.1; -;
 DR HSPF: P06601; IPDN.
 DR InterPro: IPR001523; Paired_box.
 DR Pfam: PF00292; PAX; 1.
 DR SMART: SM00351; PAX; 1.
 DR PROSITE: PS00034; PAIRED_BOX; 1.
 KM Transcription regulation; DNA-binding; Nuclear protein;
 KM Developmental protein; Paired box.
 FT NON_TER 1 126
 FT DOMAIN 2 126 PAIRED_BOX.
 SQ SEQUENCE 339 AA; 36214 MW; E57764C9C9CB54D6F CRC64;

Query Match 12.3%; Score 70; DB 1; Length 339;
 Best Local Similarity 25.8%; Pred. No. 3.4;
 Matches 31; Conservative 17; Mismatches 42; Indels 30; Gaps 5;

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OY 10 LLAGVPLSMDLPEPRSRASKIRVHSRGLMAIGHFMGKKSLEP-----SSP 57
    ||| || :|| | :| | :| | :| |
Db 104 LLAGGVCD-KYVPSV-SSISRLRNKIGNLSQGHYESYKQHQPPLPYNHITYXP 161
OY 58 SPLGTA-----PHTSLRDQRLQISH---DLGILLKKALGVSLSRAPQIQ 101
    ||: | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 162 SPLAAGAKVPTPPGVPAIPGTWAMPRTWPPSSHVTDILGIRNSITDQVSDTSSYPSPKVE 221
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Job time: 127 sec